Novel quantitative trait loci for leaf blight resistance in sorghum aids in understanding of E. turcicum pathosystem

Sarah Lipps^{1*} (slipps@illinois.edu), William Rooney², Santiago Mideros¹, **Tiffany Jamann**¹ University of Illinois, Urbana; ²Texas A&M University, College Station

Project Goals: Short statement of goals. (Limit to 1000 characters)

Decreasing yield losses due to pathogens is crucial for any crop production. Sorghum leaf blight (SLB) and northern corn leaf, both caused by *Exserohilum turcicum*, are major diseases of sorghum and maize, respectively. In sorghum, yield losses as high as 50% have been reported. In contrast to maize, genetic architecture of resistance against *E. turcicum* in sorghum is poorly understood. By dissecting the genetic architecture of resistance to leaf blight in sorghum we can better understand resistance in both maize and sorghum. We had two overall objectives: i) exploit the genetic variation in two recombinant inbred line populations to identify quantitative trait loci associated with resistance and ii) identify shared resistance genes between sorghum and maize. We identified six loci, three in each population, significantly associated with resistance to SLB. The sorghum homologs of eight previously known maize resistance genes colocalized with the sorghum QTL. By understanding host resistance in the two species, we can optimize management strategies to create more durable resistance and protect bioenergy feedstock yields.

This work is funded by DOE award number DE-SC0019189 (Plant Feedstocks Genomics).